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**DEVELOPING SELECTION CRITERIA FOR IMPROVING GRAIN YIELD OF  
EARLY MATURING MAIZE**

**BY**

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## ABSTRACT

Early maturing maize genotypes yield 15-30% less than medium-late maturing ones and improving the yield of early maturing maize is a great challenge. Grain-filling rate (GFR) and effective grain-filling duration (EGFD) are important physiological traits of maize grain yield formation. One strategy for improving grain yield of early maturing maize involves assessment of grain-filling traits as secondary traits that can aid selection for high grain yield in early maturing maize. However, exploitation of the grain-filling traits in genetic improvement of grain yield in maize has been limited by the absence of knowledge on the genetics of these traits. The aim of this study was to develop a breeding and selection criteria for improving the grain yield of early maturing maize based on grain-filling traits. The objectives of the study were to; i) determine the genetic variability of grain-filling rate and effective grain-filling duration and their association with allied traits in early maturing maize, ii) investigate the nature of inheritance of grain-filling rate and effective grain-filling duration and the associated traits in early maturing maize, and iii) identify simple sequence repeat markers for grain-filling rate and effective grain-filling duration and the related traits in early maturing maize.

A study was conducted at CIMMYT-Zimbabwe using an  $\alpha$ -lattice design with two replications to investigate the genetic variability of grain-filling traits in eighteen early maturing tropical maize inbred lines derived from CIMMYT germplasm. Highly significant differences ( $P < 0.05$ ) were observed for grain yield, 1000 grain weight (TGW), GFR, EGFD, total grain-filing duration (TGFD), kernels per rows (KR) and rows per cob (RC). There were significant differences ( $P < 0.05$ ) between the top nine and bottom nine inbred lines in terms of grain yield attributed to differences in GFR, TGFD and TGW. Path analyses showed that these grain-filling traits had huge direct effects on grain yield. The broad sense coefficient of genetic determination (the fixed parent equivalent of broad sense heritability) was above 70% for all the traits. The highest grain yield was obtained from the inbred line T032-30 (79.2 g plant<sup>-1</sup>) and the lowest from inbred line CML506 (37.6 g plant<sup>-1</sup>), respectively. A subset of these CIMMYT maize inbred lines were used in the determination of the nature of inheritance of the grain yield and grain-filling traits.

In investigating the nature of inheritance of grain-filling traits, forty-four hybrids were generated using North Carolina design II and evaluated using an  $\alpha$ -lattice design with two replications at CIMMYT-Zimbabwe under irrigated and non-irrigated environments. Highly significant differences ( $P < 0.05$ ) were observed among the hybrids for grain yield, TGW, GFR, EGFD, TGFD, KR and RC. The earliest-maturing hybrid took 127 days to reach physiological maturity and produced grain yields comparable to those of the medium-maturing genotypes ( $7 \text{ t ha}^{-1}$ ). It had a high grain-filling rate of  $2.40 \text{ g plant}^{-1}\text{d}^{-1}$  (18% higher than low-yielding hybrids), and a relatively long effective grain-filling duration. Although grain-filling rate and effective grain-filling duration were negatively correlated, several hybrids were distinctly above the trend line. Grain-filling rate and effective grain-filling duration had high coefficients of genetic determination, positive correlations with grain yield, low error terms and low genotype  $\times$  environment interactions, making them appropriate selection traits for improved grain yield. The grain-filling traits are quantitatively inherited, with the non-additive gene action being more important than additive gene action. The narrow sense heritability for grain-filling traits was low but higher than the narrow sense heritability for grain yield.

However, GFR and EGFD are difficult to measure due to the complex repeated destructive sampling needed. A total of 28 simple sequence repeat (SSR) markers were used to screen 184 testcross families derived from selfing a bi-parental cross (VL08526 X VL058014) between CIMMYT inbred line parents with contrasting grain-filling traits and test-crossed with a CIMMYT inbred line tester (CML 491) with medium GFR and medium EGFD. The testcross families were evaluated for grain yield, GFR, EGFD, kernels per row (KR) and kernel rows per ear (RC). Single marker analyses using regression analyses approach showed that five markers located on chromosome 1, 3, 5 and 10 had associations with EGFD, KR and RC ( $R^2 > 12\%$ ). Marker phi063 was associated with EGFD, KR and RC while marker phi102228 was associated with both KR and RC. Marker phi308707 was associated with KR while marker phi331888 was associated with RC. Grain yield was correlated to EGFD, KR and RC and therefore markers for EGFD, KR and RC could be used for indirect selection for yield. Overall in this study, potential inbred lines and hybrids were identified along with a selection scheme for improving the yield of early maturing maize based on grain-filling traits and/ or simple sequence repeats markers.